REMARKS

Claims 11, 13-15 and 30-34 are currently pending. In the Final Office Action mailed January 11, 2006, the Examiner has maintained the following issues, which are set forth below by number in the order they are addressed herein:

1) Claims 11 and 31-34 stand rejected under 35 U.S.C. § 112, first paragraph, as allegedly failing to comply with the written description requirement; and

2) Claim 30 stands rejected under 35 U.S.C. § 102(a) as allegedly anticipated by Hillier *et al.*, GENBANK Accession No. AA402683 (1997).

Applicants thank the Examiner for indicating that Claims 13-15 are allowed. Even so, Applicants hereby enter new Claims 35-40 in order to further the prosecution of the present application and Applicants' business interests, yet without acquiescing to the Examiner's arguments. Applicants reserve the right to prosecute the original, similar, or broader claims in one or more future application(s). The new claims do not introduce new matter. In particular, support for new Claims 35-37 can be found for instance in Example 4 and Figure 7, as well as in the description, which teaches:

> N- and C-terminal deletion derivatives of IKK-γ (SEQ ID NO:2) were generated and assayed for their ability to effect TNF-responsive and basal IKK kinase activity...both ΔN-IKK-γ (134-419) and ΔC-IKK-γ (1-300) retained the ability to interact with IKKα/β in cells (Specification, at page 21, lines 18-28).

Similarly, support for new Claims 38-40 (which are narrower in scope than pending Claims 11 and 31-34) can be found for instance in the description, which teaches:

> The term IKK-γ subunit ...also describes polypeptides having greater than about 65%, 75%, 85%, 90%, 95%, 97%, or 99% amino acid sequence identity with SEQ ID NO:2, said amino acid identity determined with CLUSTALW using the BLOSUM 62 matrix with default parameters (Specification, at page 19, lines 23-32).

Since new Claims 35-40 are of comparable or narrower scope than what has already been examined in the instant application, Applicants respectfully request that the Examiner consider the new claims in the pending Response to Final Office Action.

1) The Claims Meet The Written Description Requirement

The Examiner has rejected Claims 11 and 31-34 under 35 USC § 112, first paragraph, as allegedly failing to comply with the written description requirement for containing subject matter, which was not described in the Specification in a way as to convey that the inventors had possession of the claimed invention. Applicants respectfully disagree that the claims fail to meet the written description requirement and that the skilled artisan could not readily ascertain the structures of the claimed nucleic acids, and provide below a point-by-point rebuttal of the Examiner's written description rejection.

Regarding Applicants arguments for the patentability of Claims 11 and 31-34, the Examiner states "an assertion that compounds can be identified is not a description" (Office Action, page 2). Applicants respectfully remind the Examiner that they have provided more than a wish or a plan for obtaining an embodiment of the claimed invention. In contrast to the case law[1] cited by the Examiner in the Office Action dated June 28, 2005, in which not a single compound as recited in the claims was disclosed, Applicants have disclosed multiple nucleic acids encoding polypeptides having one or more biological activities of IKK-γ, with at least one encompassed by the claims in question. Specifically, Applicants have taught that nucleotides 149 to 1408 of SEQ ID NO:1 encode a "polypeptide with at least 90% amino acid identity to SEQ ID NO:2, wherein said peptide has one or more biological activities of a full length IKK-γ polypeptide" and thus have provided an embodiment meeting the limitations of Claims 11, 31-34 and 38-40. In addition, Applicants have provided amino-terminal and carboxy-terminal deletion mutants with homotypic and heterotypic binding activities encompassed by Claims 35-37.

The Examiner has also mischaracterized Applicants arguments regarding knowledge of one skilled in the art. Specifically, the Examiner states:

> Applicant also asserts that polypeptides sharing 378 amino acids with SEQ ID NO:2 can be easily identified because of common knowledge of conservative amino acid changes. These arguments are not persuasive because the 90% amino acid identity recited in the claims is not drawn to conservative amino acid changes (Final Office Action, page 2).

[1] *Univ. of Rochester v. G.D. Searle & Co.*, 358 F.3d 916, 927 69 USPQ2d 1886, 1894-95 (Fed. Cir. 2004).

In the first place one skilled in the art would know that the claimed nucleotides would encode polypeptides sharing at least 378 amino acids with SEQ ID NO:2 because of the "90% amino acid identity" limitation of Claims 11 and 31-34 (not based upon knowledge of conservative amino acid changes). In the second place, the claims need not be limited to conservative amino acid changes because one skilled in the art would further know that the claimed nucleic acids would encompass nucleic acids encoding polypeptides with one or a plurality of conservative amino acid changes throughout the polypeptide, as well as polypeptides with one or more non-conservative amino acid changes in region(s) of the polypeptide not required for biological activity. Even so, new Claims 38-40 have been introduced which recite "encoding an IKK-γ polypeptide comprising one or more conservative amino acid changes such that said IKK-γ polypeptide has at least 95% [97% or 99%] amino acid identity with SEQ ID NO:2."

In addition, Applicants contend one skilled in the art would know that Applicants are in possession of the claimed invention, when the knowledge of one skilled in the art is *combined* with the correlations between function and structure provided in the Specification. For instance in regard to biological activity, Applicants teach that the "human IKK-γ subunit (SEQ ID NO:2) is a polypeptide of 419 amino acids containing coiled-coil and leucine zipper α-helical regions, indicating that IKK-γ can be engaged in homotypic and heterotypic interactions" (Specification, at page 19, lines 7-11). Specifically as shown in Figures 2B and 2C, human IKK-γ is contemplated to comprise four α-helical regions, the C-terminal most comprising a leucine zipper motif with leucines at positions 322, 329, 336 and 343. In addition, Applicants teach that the carboxy-terminal residues of IKK-γ comprise a zinc finger motif comprising cysteines at positions 397, 400, 417 and a histidine at position 413 (Specification, at page 11, lines 16-20). Moreover, Applicants have demonstrated in Example 4, that even significant amino-terminal and carboxyl-terminal truncations (ΔN: deletion of residues 1-133; and ΔC: deletion of residues 301-419) of IKK-γ do not disrupt IKK-α and IKK-β binding activity of the variant IKK-γ polypeptides or their ability to form dimers and/or trimers. Taken together with common knowledge, one skilled in the art would appreciate that even polypeptides having less than 90% amino acid identity (e.g., ΔN having ~68% and ΔC having ~72% amino acid identity) with SEQ

ID NO:2, would possess one or more biological activities of a full-length IKK-γ polypeptide (e.g., binding activity).

Applicants further contend that the Examiner has too narrowly interpreted Example 9 of the revised written description guidelines in stating that this "argument is not persuasive because this example assesses whether a disclosure of a SEQ ID NO provides description of sequence that hybridize to this sequence, not to sequences sharing identity with the sequence" (Final Office Action, page 3). Applicants contend that the teachings of this example should not be limited to hybridization claims since the recitation of hybridization conditions is simply a means for defining structural similarity. Likewise, the phrase "having at least 90% amino acid identity with SEQ ID NO:2" is a means for defining structural similarity of the claimed nucleic acid molecules. In fact, the percent identity language arguably narrows the claims more than the hybridization language, in that a probe may hybridize to a nucleic acid target sequence with a local region of high homology, but with a low overall percent identity.

Furthermore, in regard to Applicants comparison of the pending claims to those of numerous issued patents, the Examiner simply states that this "argument is not persuasive because each application is assessed on its own merits' (Final Office Action, page 3). In the first place, Applicants specifically cited U.S. Patent No. 6,590,077 to Tarczyniski *et al.* ('961 Patent, with Andrew Wang as the Primary Examiner). Like the instant application, the '961 Patent claims a genus of nucleic acids described by percent identity to a given SEQ ID NO, with a disclosure of a species of the claimed genus. Specifically, the '961 Patent claims "a polynucleotide having at least 70 percent sequence identity to SEQ ID NOS:1 or 3" (See, '961 Patent Claims 1, 8, 11, 13, 17, and 29). For the sake of clarity, Applicants contend that the Examiner should address this argument by describing the specific merits of the '961 Patent that has entitled Tarczyniski *et al.* to a greater claim breadth than that which the Examiner is willing to allow Applicants.

In summary, Applicants believe that the arguments and evidence (e.g., citations to the Specification) provided above obviate the written description rejection, and accordingly request that this rejection be withdrawn. Applicants encourage the Examiner to confer with her Supervisory Patent Examiner (SPE) as needed to specifically address each point raised by Applicants. In addition, should the Examiner maintain the written description rejection, than

Applicants respectfully request that appropriate amendments to the claims be suggested which would result in their allowance (See, MPEP 2163.04).

2) The Claims Are Novel

The Examiner has rejected Claim 30 under 35 U.S.C. § 102(a) as allegedly anticipated by Hillier *et al.*, GENBANK Accession No. AA402683 (Hillier). According to the Examiner:

> Applicant states that the claimed antisense comprises nucleotide sequences not disclosed by Hillier *et al.* and the claim is thus novel. This argument is not persuasive because the claim uses the open language comprising and the sequence of Hillier *et al.* is complementary to a sequence within the recited range (Final Office Action, page 3).

Applicants respectfully disagree that the invention is anticipated by Hillier, and contend that the Examiner's continued rejection of Claim 30 demonstrates a lack of understanding of the law, as well as a failure to properly analyze the amended claim before maintaining this rejection. The Examiner is reminded that "to anticipate a claim, the reference must teach every element of the claim" (MPEP, 2131). A comparison of the claimed invention to that of Hillier clearly indicates that Hillier does not teach or suggest a nucleotide sequence complementary to nucleotides 149 to 1405 of SEQ ID NO:1. A sequence alignment of SEQ ID NO:1 with the EST of Hillier (e.g., as provided in Paper 8 of the Office) indicates that the only residues shared between the claimed antisense nucleotide and Hillier is the TAG stop codon corresponding to residues 1406 to 1408. Applicants use of the open "comprising" claim language in Claim 30 is irrelevant to this rejection, since Hillier fails to disclose ~1.3 kb of the claimed antisense polynucleotide. Additionally, Applicants draw the Examiners attention to the fact that rejected Claim 30 is directed to an isolated antisense strand, and thus is narrower than allowed Claim 14, which encompasses sense, antisense and double stranded nucleic acid molecules. Thus, Applicants request that this rejection be withdrawn.

CONCLUSION

Applicants believe the amendments and arguments set forth above traverse the Examiner's rejections and, therefore request that a timely Notice of Allowance be issued in this case. However, should the Examiner believe that a telephone interview would aid in the prosecution of this application, Applicants encourage the Examiner to call the undersigned collect.

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